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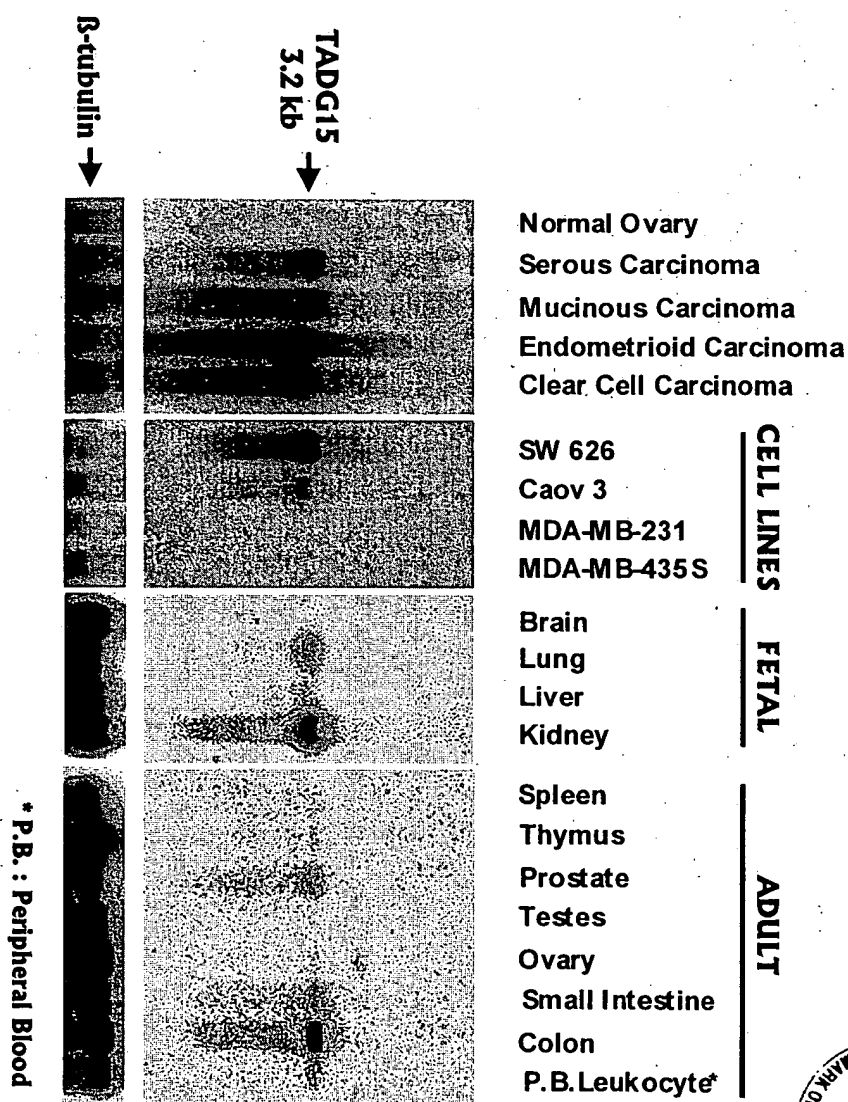


Fig. 5

APPROVED	O.G. FIG.
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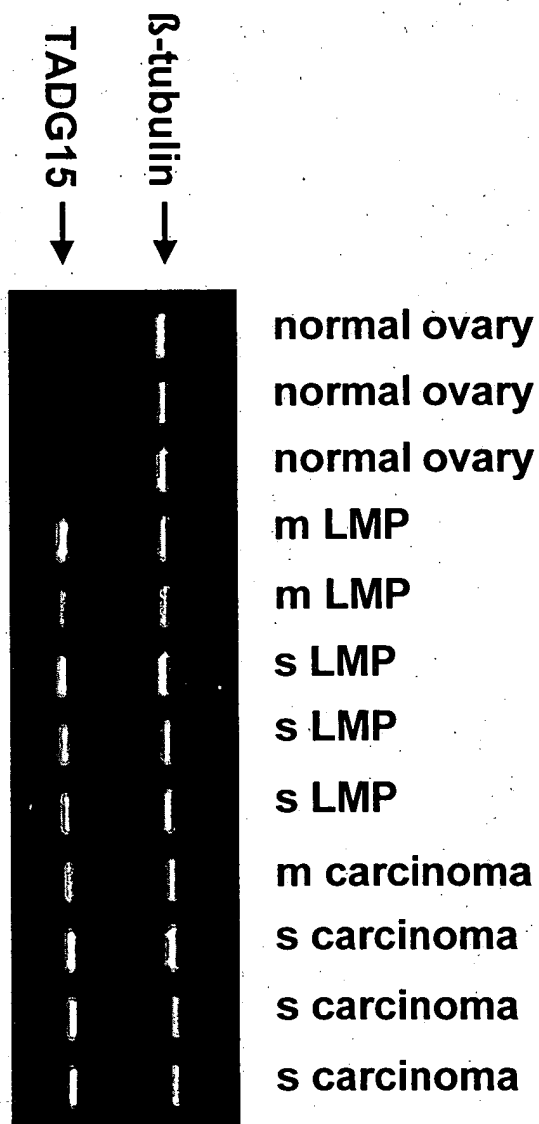


Fig. 6A

APPROVED	O.G. FIG.	
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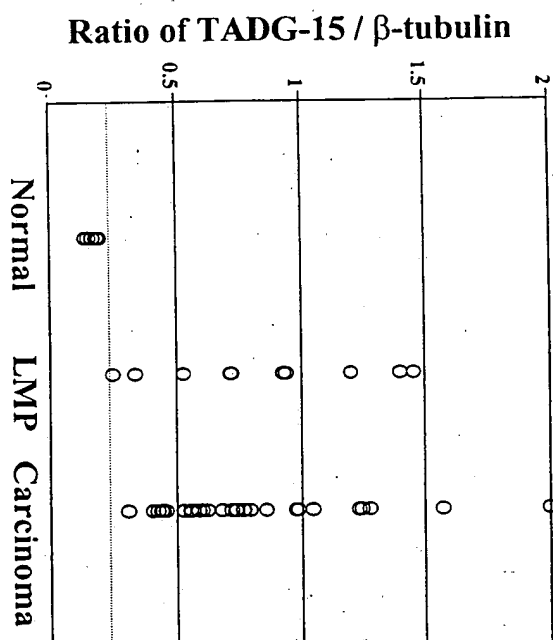


Fig. 6B

APPROVED	O.G. FIG.	<b>RECEIVED</b>
BY DRAFTSMAN	CLASS	

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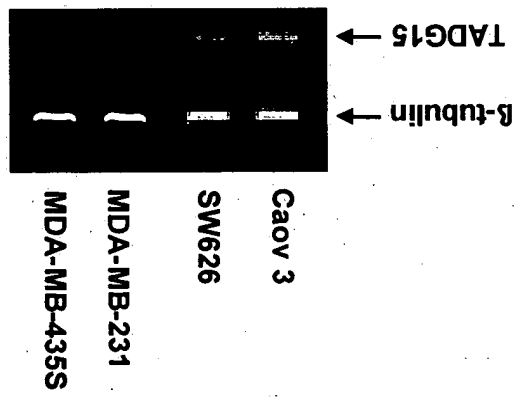
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Fig. 8



Fig. 7



APPROVED	O.G. FIG.
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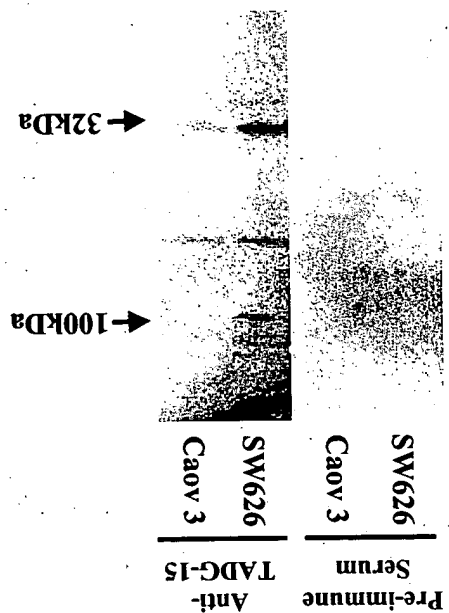


Fig. 9

APPROVED	O.G. FIG.
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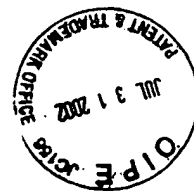


Fig. 10C

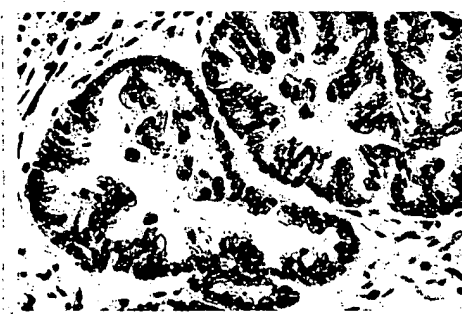


Fig. 10B

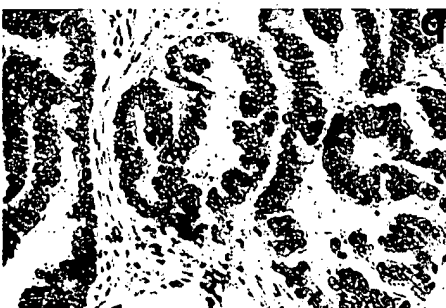


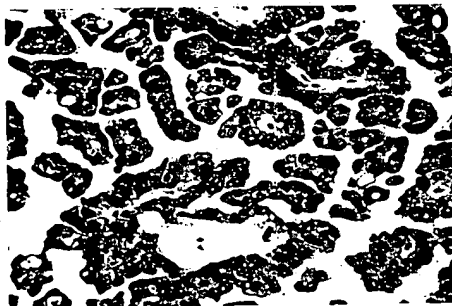
Fig. 10A



Fig. 10E



Fig. 10D



APPROVED	O.G. FIG.
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APPROVED	O.G. FIG.
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HTADG15 MGSDBARKKG GGPKEFGAGL KYNSRHEKN GIEGVEFLP VANNVKKVEKH 50  
MEPI THIN ---N-G--A- --SQ----- --D-L-NM- -F----- A--A-----R  
HTADG15 GPGRWVTLAA VLIGILLVLL GIGELVWHLQ YRDVAVQKVE NGYMLITNEN 100  
MEPI THIN --R-----V- --FSF--IS- MA-L-----EH --N-----HL-----I  
HTADG15 FVDAYENSNS TEFVSLASKV KOALKLXSG VPFLGPYHKE SAVTAFSEGS 150  
MEPI THIN -L-----T- ---I-----Q- -E-----NE --V-----K -----  
HTADG15 VIAYYWESES IPQELVEEAE RVMAEERVVM LPPRABLSKS FVVTSVVAEP 200  
MEPI THIN -----P--A--VD -A--V-----T -----A-----L-----  
HTADG15 TDSKTVQRTQ DNSCSFGLHA RGVELMRFTT PGFPDSPYPA HARCQWALRG 250  
MEPI THIN I-PRML-----A---- H-AAVT-----N-----V----  
HTADG15 DADSVLSLTF RSEDLASCODE RGSDIVTVYN TLSPEMPEHAL VOICGTYPFS 300  
MEPI THIN -----V-P--- H-----D S-----V -R----FS--  
HTADG15 YNLTEHSSON VLLITLITNT ERHPGFEAT FFQLPMMSSC GGRIRKAQGT 350  
MEPI THIN ----L-----F-V----- G---L-----K-----V-SDT---  
HTADG15 ENSPYYPGHY PENIDCTWNI EVNNQHVAV SEKEFYILLEP GVPAGTCPEKD 400  
MEPI THIN -S-----N-----K-----RN--- R--L---VD- N--V-S-T--  
HTADG15 YVEINGEKYC GERSQFVVS NSNKITVRFH SDQSYTDIGF LAEYLSYDSS 450  
MEPI THIN -----GS -----S- --S---H-- --H-----N

Fig. 11A



APPROVED	O.G. FIG.
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HTADG15 DPCPGQETCR TGR CIRKEIR CDGNADCTDH SDEINCSDA GHQFTCKNKE 500  
MEPI THIN -----M-M-K -----P-Y ---RY-R-N-T-----Q-

HTADG15 CKPEFWCDS VANDCDNSDE QGCSCPAQTF RCSNGKCLSK SQQCNKDDC 550  
MEPI THIN -----G---E-----GS-K-----PQ--K-----N-

HTADG15 GDGSDASCP KVNVTCTKH TYRCLNGICL SKGNPECDGK EDCSDGSDER 600  
MEPI THIN -----D S---S---Y ---Q-----T-----

HTADG15 DCDGCLRSFT RQARVVGCTD ADEGEWPMQV SLHALGQGH CGASLISPNT 650  
MEPI THIN N-----K-----N-----L-----D-

HTADG15 LVSAHXYID DRGRYSDEP QWTAFLGLHD QSQRAPGVQ ERLKRIISH 700  
MEPI THIN -----FQ--KN-K---Y-M-----L--K---S---LK-----T-

HTADG15 PFNDFTFDY DIALLEIEKP AEYSSMVRPI CLPDASHVFP AGKAIWVTGM 750  
MEPI THIN -S-----S V---TV-----T-----

HTADG15 GHTQYGTGA LILQKEIRV INQTCENIL PQQITPRMVC VGFLSGVDS 800  
MEPI THIN ---KE-----D-M-----

HTADG15 CQGDSSGPLS SVEADGRIFQ AGVSWGDC AQRNKEGYT RLPLEFDWIK 850  
MEPI THIN -----A-K--M-----E-----CSSGLDQ

HTADG15 ENTGV\* 900  
MEPI THIN RAHWGIAAWT DSRPQPTPTGM PDMHTWIGER NTDDIYAVAS PQHNPDCEL

HTADG15 SEQ ID NO: 2  
MEPI THIN HP SEQ ID NO: 10 902

Fig. 11B

APPROVED	O.G. FIG.
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TADG15: TCAAGAGCGCCCTCGGGGTAACATGGGAGAGCATCGGCCCCGGAAGGGCGGAGGGGGCCGGAAGAGACTTCGGCGCGGGACT 81

SNC19: .....

82 CAAGTCAACTCCCGGACAGAGAAAGTAAATGGCTTGAAGAGAGCGGTGAGATTCTCCAGTCAACACGTCAAGAAAGTGAAGAAAGCATGGCCCCGGGG

.....

182 CGCTGGGTGTGCTGGACGCCGTGTGATCGGCCCTCTTGTGCTTGTGGGGATCGGCTTCCTGTGTGTCATTTGCAAGTACCGGGACGTGCTGTC 281

1 CGCTGGGTGTGCTGGACGCCGTGTGATCGGCCCTCTTGTGCTTGTGGGATCGGCTTCCTGTGTGTCATTTGCAAGTACCGGGACGTGCTGTC 100

282 AGAAGCTCTCAATGCTTACATGAGATCACAATGAGAAATTTTGTGATGCTTACAGAACTCCAATCCTAGTTTGTAAAGCTTGCCAGCAAGT 381

101 AGAAGCTCTCAATGCTTACATGAGATCACAATGAGAAATTTTGTGATGCTTACAGAACTCCAATCCTAGTTTGTAAAGCTTGCCAGCAAGT 200

382 GAAGAGCGGCTGAAGCTGCTGTACAGCGAGATCCATTCTGGGCCCTTACCACAAGAGATCGGCTGTGACGGCTTTCAGCGAGGGCGAGCTCATGCCC 481

201 GAAGAGCGGCTGAAGCTGCTGTACAGCGAGATCCATTCTGGGCCCTTACCACAAGAGATCGGCTGTGACGGCTTTCAGCGAGGGCGAGCTCATGCCC 300

482 TACTACTGTCTGAGTTGACATGCCGAGACCTGTGTGAGAGAGCCGAGCGCGTCAATGCGGAGAGCGCGTATGTCATGCTGCCCGCGGGCGCGCT 581

301 TACTACTGTCTGAGTTGACATGCCGAGACCTGTGTGAGAGAGCCGAGCGCGTCAATGCGCGTCAATGCTGCCCGCGGGCGCGCT 399

582 CCCTGAAGTCTTGTGTGATCACTGATGAGGCTTTCCCGAGGACTCCAAAACAGTACAGAGACCCAGGACAAACAGCTGACGCTTTGGCTGACGCG 681

400 CCCTGAAGTCTTGTGTGATCACTGATGAGGCTTTCCCGAGGACTCCAAAACAGTACAGAGACCCAGGACAAACAGCTGACGCTTTGGCTGACGCG 498

Fig. 12A

APPROVED	O.G. FIG.
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682 CCGCGGTGTGAGCTGATGCGGCTTCAACAGCCCGGCTTCCCTGACAGCCCTTACCCCGCTCATGCCCCGCTGCGAGTGCGGCCCTTGCGGGGAGCCCGAC 781  
|||||  
499 CCGCGGTGTGAGCTGATGCGGCTTCAACAGC. CCGGCTTCCCTGACAGCCCTTACCCCGCTCATGCCCCGCTGCGAGTGCGGCT... TCGGGGAGC. CGAC 592  
782 TCAGTGTGAGCTTCACTTC... CGAGCTTGTGACCTTGCGCTTCCGACGAGCGCGGAGCAGCTGTGACGCTGTACAAACCTTGAGCCCAT 876  
|||||  
593 GCAGTGTGAGCTTCACTGAGCTGACCTGACG. TTGACTGCGCT... CGAGGAGCGCGGAGCAGCTGTGAC. GTGTACAAACCTTGAGCCCAT 686  
877 GGAGCCCAAGCCCTGTGAGCTGTGTGTGAGCCTTCCCTTCAACCTTGTGACCT. CCTTCCA. GAAGCTTGTGTATCATCACTGATTA 974  
|||||  
687 GGAGCCCAAG. CCTGTG. AGTGTGTGAGCCTTCCCTTCAACCTTGTGACCTTCCCTTCCAGAACGTCTGTATCATCACTGATTA 783  
975 CCACACTGAGCGCGGCTTCCGCTTTGAGGCCACCTTCTTCCAGCTGCTAGATGAGCAGCTGTGAGCGCGCTTACGTAAAGCCCAAGGACATT 1074  
|||||  
784 CCACACTGA. CCGGCTTCCGCTTTGAGGCCACCTTCTTCCAGCTGCTAGATGAGCAGCTGTGAGCGCGCTTACGTAAAGCCCAAGGACATT 881  
1075 CAACAGCCCTTACTTACCAAGGCTGACCTTCAACCTTGTGACCTGACATGAACTTGTGAGTGTGCGCCCAACAGCAGATGTGAAGGTTCATAATTTC 1174  
|||||  
882 CAACAGCCCTTACTTACCAAGGCTGACCTTCAACCTTGTGACCTGACATGAACTTGTGAGTGTGCGCCCAACAGCAGATGTGAAGGTTCATAATTTC 981  
1175 TTCTACTGTGTGAGCCCGGCTGTGCTGCGGCTTCCCAAGGACTACCTGTGAGATCAATTGGGAGAAATGCTGCGAGAGAGGTCCCACTTCGTCG 1274  
|||||  
982 TTCTACTGTGTGAGCCCGGCTGTGCTGCGGCTTCCCAAGGACTACCTGTGAGATCAATTGGGAGAAATGCTGCGAGAGAGGTCCCACTTCGTCG 1081  
1275 TCACAGCAACAGCAACAGATACAGTTCCTTCCACTGACATGACCTTCAACGAGACAGCGGCTTCTTGTAGCTGAATACCTTCTTCAAGACTCCAGTGA 1374  
|||||  
1082 TCACAGCAACAGCAACAGATACAGTTCCTTCCACTGACATGATCACTTCAACGAGACAGCGGCTTCTTGTAGCTGAATACCTTCTTCAAGACTCCAGTGA 1181

Fig. 12B



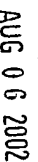
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1375 CCCATGCCCGGGGAGTTTCACGTGCCCGCACGGGGCGGTGTATCCGGAAGAGACTGCCCTGTGATGGCTGGGGCCACTGCACCGCACAGGAGTACGCTC 1474  
|||||  
1182 CCCATGCCCGGGGAGTTTCACGTGCCCGCACGGGGCGGTGTATCCGGAAGAGACTGCCCTGTGATGGCTGGGG .CGACTGCACCGCACAGGAGTACGCTC 1290  
1475 AACTGCAGTTGCCAGCGCGGCCACCACTTACGTGCACGAACAAGTTCTGCAAGCCCTCTTCTGGGTGCGACAGTGTGAACGACTGCGGAGACACA 1574  
|||||  
1281 AACTGCAGTTGCCAGCGCGGCCACCACTTACGTGCACGAACAAGTTCTGCAAG . .CTCTTCTGGGTGCGACAGTGTGAACGACTGCGGAGACACA 1377  
1575 GCGACGAGCAGGGGTGCAAGTTGCCG .CCGACACTTACAGTGTCCCAATGGGAAGTCCCTCTCGAAAAGCCAGCAGTCAATGGGAAGGAGCAGTGTG 1673  
|||||  
1378 GCGACGAGCAGGGGTGCAAGTTGCCGACCCAGACTTTCAGTGTCCCAATGGGAAGTCCCTCTCGAAAAGCCAGCAGTGTGAACGACTGCTGTG 1477  
1674 GGGACGGGTCCGACGAGGCTCTCTGCCCAAGTGAACGTGTACTTACCACACACACTTACGCTGCTCAATGGGCTTGTGAGCAAGGGCAA 1773  
|||||  
1478 GGGACGGGTCCGACGAGGCTCTCTGCCCAAGTGAACGTGTACTTACCACACACACTTACGCTGCTCAATGGGCTTGTGAGCAAGGGCAA 1577  
1774 CCTGAGTGTGACGGGAAGAGACTGTAGCGACGGCTCAGATGAGAAGACTGCGACTGTGGGCTGCGGCTCATTCACGAGCAGGCTCGTGTGTGGG 1873  
|||||  
1578 CCTGAGTGTGACGGGAAGAGACTGTAGCGACGGCTCAGATGAGAAGACTGCGACTGTGGGCTCGGCTCATTCACGAGCAGGCTCGTGTGTGGG 1677  
1874 GGCACGGATGCGGATGAGGGCGAGTGGCCCTGCGAGGTAAAGCTGTGATGCTGTGGGCCAGGGCCACATCTGCGGTCTTCCATCTTCCCAACTGGC 1973  
|||||  
1678 GGCACGGATGCGGATGAGGGCGAGTGGCCCTGCGAGGTAAAGCTGTGATGCTGTGGGCCAGGGCCACATCTGCGGTCTTCCATCTTCCCAACTGGC 1777  
1974 TGGTCTCTGCGCACACTGTGATGATGACAGAGGATTTCAGTGTGAGACCCACGACAGTGAAGGGCTTCTGCGGCTTGCACGACAGCCAGCG 2073  
|||||  
1778 TGGTCTCTGCGCACACTGTGATGATGACAGAGGATTTCAGTGTGAGACCCACGCA . .GGAAGGCTTCTGCGGCTTGCACGACAGCCAGCG 1875

Fig. 12C



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[illegible]

**Fig. 12D**

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2771 AGTGAGCTGGG. GGTGAAGGGAGG. AACTGTGTCTTACTGACCAACTGGGGCAAAAGTTGAAGACACACCTCCCCCAAGCCCAAGC 2868
|||||
2568 AGTGAGCTGGAGGGTGAAGGGAGGAACACTGTGTCTTACTGACCAACTGGGG. CAAGTTGAAG. CACAG... CTCGGCAGCCC.. AAG 2658
|||||
2869 TGGCCGAGGCGCTTGTGTATATCTGCTCCCTGTCTGTAGAGACAGCGGGAACGAGCTTCGAGCCTCTCAGTGAAGTGTGGGCTGCCG 2968
|||||
2659 TGGCGAGGACGCGCTTGTGTGATA. CTGCC. CTGCTGTATACAGGGAAGACCTGA..... TCTCTAGTGA..... GTGTGACTGCCG 2735
|||||
2969 ATCTGGGCTGTGGGCCCCCTGGGCCACGCTCTTGAAGAAAGCCAGCTCGAGAGACCCCTGGAAAAACAGAGGGGTCTGAGACTGAATTTTACCAGCT 3068
|||||
2736 ATCTGG... CTGTGTCTTGGCCAGCTCTTGAAGAAAGCCAGCTCGAGAGACCCCTGGAAAAACAGAGGGGTCTGAGACTGAATTTTACCAGCT 2832
|||||
3069 CCCAGGCTGACTTCAGTGTGTGTATTTGTGTAAATGGGTAAACATTTATTTTAAAAA 3147 (SEQ ID NO: 1)
|||||
2833 CCCAGG... TGACTTCAGTGTGTGTA. TTGTAAATGAGTAAAAACATTTTATTTTAAAAA 2900 (SEQ ID NO: 9)

```

Fig. 12E

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Fig. 10C

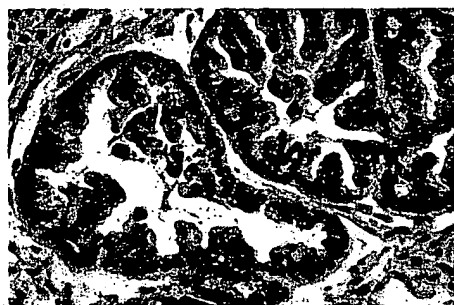


Fig. 10B



Fig. 10A





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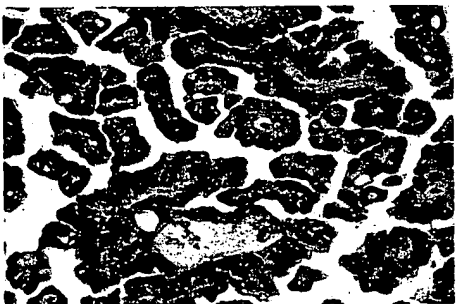


Fig. 10D

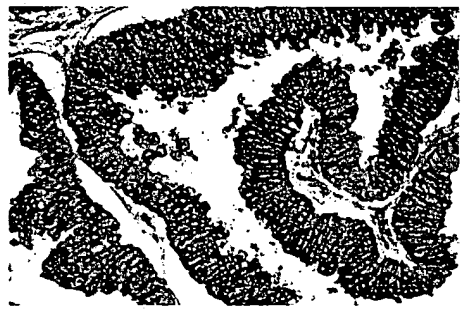


Fig. 10E



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Fig. 10C

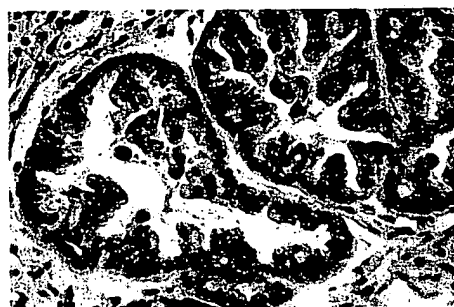


Fig. 10B

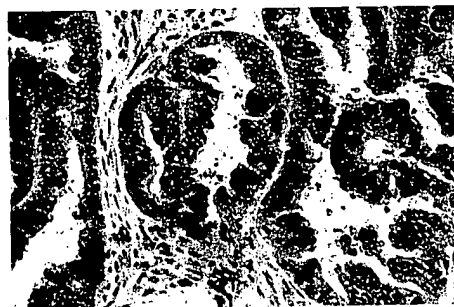


Fig. 10A





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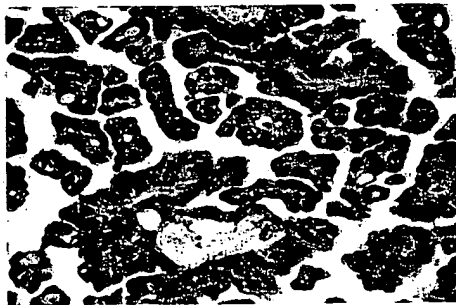


Fig. 10D



Fig. 10E